

DNA 'barcode' revealed in plants

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A "barcode" gene that can be used to distinguish between the majority of plant species has been identified, say scientists.

This gene can be used to catalogue plant life as it has a slightly different code between species but is nearly identical within a species.

Species that look the same to the human eye can be told apart with a small leaf sample.

DNA barcoding is already a well-established technique in animals.

The work is reported in the Proceedings of the National Academy of Sciences journal.

Co-author Dr Vincent Savolainen, from Imperial College London and the Royal Botanic Gardens Kew told the BBC News website: "It was our dream to find the gene in plants that could identify species.

"We found that a small gene, gene matK located in the chloroplast of the plant, has enough variation to identify between species but is nearly identical in plants of the same species."

Work over the last few years has shown the chloroplast, the area involved in photosynthesis, is a good place to look for a barcode gene.

Rates of change

Dr Savolainen explains: "Nuclear genes usually evolve too rapidly to distinguish between the same species, but chloroplast genes evolve at a slower rate, allowing for this, yet fast enough for differences to occur in the DNA code between species."

He added: "The chloroplast is also a good place to work technically."

Animal barcoding too uses a gene found outside the nucleus, the CO1 gene. This is found in the microscopic powerhouses of a cell - its mitochondria.

While the plant barcode gene will not be able to identify every plant species on Earth, it is most likely to be able to distinguish between 90% of them.

Dr Savolainen explains why: "In the case of very rapid bursts of speciation, matK may not record enough variation between species.

"Also hybrids have their genome rearranged, which may confuse the information provided by matK."

Hybridisation, where species cross-breed, is much more common in plants than animals and therefore a bigger problem when sequencing at the barcode gene in plants.

Dr Savolainen says: "To find this plant DNA barcode gene we compared eight potential barcodes and looked at plants in two of the 25 biodiversity hotspots in the world, in over two different continents for two different habitats."

The team analysed around 1,600 samples taken from the tropical forests of Costa Rica, which has one of the richest orchid floras of the world and the temperate tree and shrub land of Kruger National Park in South Africa.

Cryptic species

In addition, Dr Savolainen's team have used the matK gene to identify around 1,000 species of orchid in the tropical forests of Costa Rica. Orchids are well known to be difficult to identify because they look similar, particularly when sterile.

DNA barcoding provides an additional taxonomic tool when traditional observation techniques are unreliable.

They are also helpful in revealing cryptic species: those which look the same but are in fact genetically different.

"Using the matK gene we found what was previously assumed to be one species of orchid was actually two," says Dr Savolainen.

He hopes that, in the long-run, a genetic database of the matK DNA for as many plant species as possible will be built up, so that samples can be compared to this database and difficult plant species accurately identified.

Instantaneous identification

"In the future we hope that non-experts will be able to take a small portable device, capable of reading a plant's genetic barcode, into species rich areas of the world for their plant composition to be established," he says.

Currently, there are only a few experts that could accurately identify the plant composition of biodiverse hotspots in the world so that a device like this would dramatically increase the pace of such work.

He also believes that as sequencing technology gets faster and cheaper, devices at ports and airports could provide the conservation benefit of checking if illegal species are being transported.

Controversy

DNA barcoding is not without its controversy, most of which rests on the fact that species identification is based on one single non-nuclear gene.

Dr Dasmahapatra, an evolutionary biologist from University College London told the BBC News website: "It [bar-coding] can be made more reliable if supplemented with information from one or more nuclear genes.

"This would reduce the problem of reliance on a single gene and help identify cases where non-nuclear DNA behaves differently to the nuclear genome."

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